

QY 314 MVH VAYSLCLP MRRSRERYLFLN MAYQQV HAN IENSWNEEEVVR IEMYISFGIMSLG LSL 373

Db 1 MVHVSCLCLPMRSEYFLNMAVQOVHANISNNEEVWRIEMVTSFGINSGLLSL 60  
 QY 374 LAVTSPSVSNALNWRFSFIQSTGLGYVALLISTFHVLYGWKRAFEDEYRYTPPNFV 433  
 Db 61 LAVTSPSVSNALNWRFSFIQSTGLGYVALLISTFHVLYGWKRAFEDEYRYTPPNFV 120  
 QY 434 LALVPSIVILDLQLCRYPD 454  
 Db 121 LALVPSIVILDLQLCRYPD 141

## RESULT 2

US-08-487-886-2

Sequence 2, Application US/08487886

Patent No. 5744448

GENERAL INFORMATION:

APPLICANT: Kelton, Christie Ann

APPLICANT: Schweickhardt, Rene Lynn

APPLICANT: Cheng, Shirley Vui Yen

APPLICANT: Nugent, No. 5744448een Patrice

TITLE OF INVENTION: Human Follicle Stimulating

TITLE OF INVENTION: Hormone Receptor

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Stephan P. Williams,

ADDRESSEE: Ares-Serono, Inc.

STREET: Exchange Place, 37th floor

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density

COMPUTER: IBM PS/2, model 55 SX

OPERATING SYSTEM: MS-DOS version 4.0

SOFTWARE: VAX/VMS Massll via Kermit to IBM MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,886

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/670,085

FILING DATE: 15-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Williams, Stephan P.

REGISTRATION NUMBER: 28546

REFERENCE/DOCKET NUMBER: US/252

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 723-1300

TELEFAX: (617) 723-8923

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 695

TYPE: Amino acid

TOPOLOGY: Linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: signal sequence

LOCATION: -17 to -1

IDENTIFICATION METHOD: hydrophobic

FEATURE:

NAME/KEY: putative amino-terminal extracellular domain

LOCATION: 1 to 349

IDENTIFICATION METHOD: similarity with other

IDENTIFICATION METHOD: dimeric glycoprotein receptor extracellular

IDENTIFICATION METHOD: domains, hydrophilic

FEATURE:

NAME/KEY: transmembrane domain

LOCATION: 350 to 613

IDENTIFICATION METHOD: similarity to other G

IDENTIFICATION METHOD: protein-coupled receptor transmembrane domains

FEATURE:

NAME/KEY: putative transmembrane region I

LOCATION: 350 to 370  
 IDENTIFICATION METHOD: similarity to other G  
 IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
 IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
 FEATURE:  
 NAME/KEY: putative transmembrane region II  
 LOCATION: 382 to 404  
 IDENTIFICATION METHOD: similarity to other G  
 IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
 IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
 FEATURE:  
 NAME/KEY: putative transmembrane region III  
 LOCATION: 427 to 448  
 IDENTIFICATION METHOD: similarity to other G  
 IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
 IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
 FEATURE:  
 NAME/KEY: putative transmembrane region IV  
 LOCATION: 469 to 491  
 IDENTIFICATION METHOD: similarity to other G  
 IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
 IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
 FEATURE:  
 NAME/KEY: putative transmembrane region V  
 LOCATION: 512 to 533  
 IDENTIFICATION METHOD: similarity to other G  
 IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
 IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
 FEATURE:  
 NAME/KEY: putative transmembrane region VI  
 LOCATION: 557 to 580  
 IDENTIFICATION METHOD: similarity to other G  
 IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
 IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
 FEATURE:  
 NAME/KEY: putative transmembrane region VII  
 LOCATION: 592 to 613  
 IDENTIFICATION METHOD: similarity to other G  
 IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,  
 IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length  
 FEATURE:  
 NAME/KEY: putative carboxy-terminal intracellular  
 NAME/KEY: domain  
 LOCATION: 614 to 678  
 US-08-487-886-2

Query Match

Best Local Similarity 4.6%; Score 107.5; DB 1; Length 695;

Matches 84; Conservative 77; Mismatches 148; Indels 185; Gaps 17;

QY 79 HEDALTKTNIEFVAJHREHYTSLWDLRHLLVG-----KILIDVSNMR 121  
 Db 98 HEIRIEKANNL-LYINPEAFQNLPLNYLLISNTGIKHLDPVHKIHSLOKVLDDIQDN 156  
 QY 122 INQYPSNAEYLASLFPDPSLIVKGFVYSAMALQGLPKDASRQVYCSNNIQRQVIEL 181  
 Db 157 IH-----TIERNSEFVGLSFESVILWL-----NNGIOEIHNC----- 189  
 QY 182 ARQLNFIPIDGLSLSAREIENLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYAR 241  
 Db 190 ---FNGTQDLDELNLSDNNNLELPNDVFGASGVPILDIRTRIHSLSYGLENLKLLRA 246  
 QY 242 NQOSDFYKIPIEIVNKL-PIVAITLLSLVY----- 271  
 Db 247 RSTYNLKKLP-----TLEKLVALMEASLTYPSCAFANRRRQISELHPICNKSILROE 300  
 QY 272 -----LAGLLAAAYOLYYGTYKRRF-----PPWLETWLCRQOL 305  
 Db 301 VDYMTQTRGQRSSLAEDNESSYRGFDITYEFDLCNEVVVDVTCSPKPAFNPCEIM 360  
 QY 306 G-----LLSFFFMVHVA-----YSLCLPMRSEYFLNMAVQOVHANIE 347